

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 17:51:48 ; Search time 31 Seconds

(without alignments)
1154.677 Million cell updates/sec

Title: US-10-005-691-2

Perfect score: 4351

Sequence: 1 MFTVSCSKMSIVDRDSS.....QQLSRHRTSLPDPKVPQ 846

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4351	100.0	846	3	US-08-885-291-55	Sequence 55, Appl
2	4351	100.0	846	3	US-09-107-847-2	Sequence 2, Appl
3	4351	100.0	846	3	US-09-496-672-55	Sequence 55, Appl
4	4149.5	95.4	855	2	US-08-816-693A-2	Sequence 2, Appl
5	4149.5	95.4	855	3	US-08-885-291-2	Sequence 2, Appl
6	4149.5	95.4	855	3	US-09-496-672-2	Sequence 2, Appl
7	4149.5	95.4	855	4	US-09-618-425-11	Sequence 11, Appl
8	1966.5	45.2	824	2	US-08-785-310A-7	Sequence 7, Appl
9	1960.5	45.1	824	3	US-08-885-291-52	Sequence 52, Appl
10	1960.5	45.1	824	3	US-09-496-672-52	Sequence 52, Appl
11	1957.5	45.0	824	2	US-08-816-693A-52	Sequence 52, Appl
12	1948	44.8	816	2	US-08-785-310A-8	Sequence 8, Appl
13	1941	44.6	816	2	US-08-816-693A-53	Sequence 53, Appl
14	1941	44.6	816	3	US-08-885-291-53	Sequence 53, Appl
15	1941	44.6	816	3	US-09-496-672-53	Sequence 53, Appl
16	1916.5	44.0	747	2	US-08-816-693A-51	Sequence 51, Appl
17	1916.5	44.0	747	3	US-08-885-291-51	Sequence 51, Appl
18	1916.5	44.0	747	3	US-09-496-672-51	Sequence 51, Appl
19	457	10.5	626	4	US-08-971-188-10	Sequence 10, Appl
20	457	10.5	626	4	US-09-374-454-21	Sequence 21, Appl
21	437.5	10.1	625	4	US-09-618-425-13	Sequence 13, Appl
22	430	9.9	789	4	US-08-971-188-9	Sequence 9, Appl
23	430	9.9	789	4	US-09-374-454-22	Sequence 22, Appl
24	424.5	9.8	602	4	US-09-637-454-19	Sequence 19, Appl
25	412.5	9.5	1507	4	US-09-914-259-37	Sequence 37, Appl
26	405.5	9.3	870	1	US-08-785-241-4	Sequence 4, Appl
27	405.5	9.3	870	4	US-09-374-454-6	Sequence 6, Appl

28	396.5	9.1	875	1	US-08-785-241-5	Sequence 5, Appl
29	395	9.1	813	4	US-09-438-833-12	Sequence 12, Appl
30	395	9.1	826	1	US-08-785-241-6	Sequence 6, Appl
31	395	9.1	826	2	US-08-480-473B-2	Sequence 2, Appl
32	395	9.1	826	3	US-08-915-213-2	Sequence 2, Appl
33	395	9.1	826	3	US-09-148-547-2	Sequence 2, Appl
34	395	9.1	826	3	US-09-235-217-2	Sequence 23, Appl
35	395	9.1	826	4	US-09-380-662-23	Sequence 1, Appl
36	395	9.1	826	4	US-09-438-833-1	Sequence 330, App
37	395	9.1	826	4	US-09-702-705-330	Sequence 330, App
38	395	9.1	826	4	US-09-736-457-330	Sequence 2, Appl
39	395	9.1	826	4	US-09-383-581-2	Sequence 2, Appl
40	395	9.1	826	5	PCT-US96-10251-2	Sequence 8, Appl
41	386.5	8.9	631	4	US-08-971-188-8	Sequence 2, Appl
42	385.5	8.9	652	4	US-09-438-833-5	Sequence 5, Appl
43	385.5	8.9	810	1	US-08-785-241-7	Sequence 7, Appl
44	384.5	8.8	485	4	US-09-374-454-4	Sequence 4, Appl
45	382	8.8	805	2	US-08-480-473B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-885-291-55
; Sequence 55, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A 100%
; EARLIER FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693 / 9616
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 55
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-885-291-55

Query Match	100.0%;	Score 4351;	DB 3;	Length 846;
Best local Similarity	100.0%;	Pred. No. 0;		
Matches 846;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFTVSCSKMSIVDRDSSIFDGLVEEDDKDKAKRYSRNKSEKKRDQFNVLIKELGSM 60		
DB	1	MFTVSCSKMSIVDRDSSIFDGLVEEDDKDKAKRYSRNKSEKKRDQFNVLIKELGSM 60		
QY	61	LPGNARKMDKSTVLQKSIDFLRKHKETAOSDASEIRQDWKPTFLSNEFTQMLTALDG 120		
DB	61	LPGNARKMDKSTVLQKSIDFLRKHKETAOSDASEIRQDWKPTFLSNEFTQMLTALDG 120		
QY	121	FFLAIMTDSILTVSESVTSLEHLPSDLDVQSIENFPEGEHSEVYKILSTHLESDSL 180		
DB	121	FFLAIMTDSILTVSESVTSLEHLPSDLDVQSIENFPEGEHSEVYKILSTHLESDSL 180		
QY	181	TPEYLKSKNOLFECCHMLRGTIDPKPESTYEVYKFIGNFKSLNSVSSAHNGFEQTQRT 240		
DB	181	TPEYLKSKNOLFECCHMLRGTIDPKPESTYEVYKFIGNFKSLNSVSSAHNGFEQTQRT 240		
QY	241	HRSYEDRVCFATVRLATPOFIKEMCYEENNEEFTSRHSLEWKFLLDHRAPPIGYL 300		
DB	241	HRSYEDRVCFATVRLATPOFIKEMCYEENNEEFTSRHSLEWKFLLDHRAPPIGYL 300		
QY	301	PREVLGTSGDYHHVDLENLAKCHEHLMQYKSKCYRFLTKGQOMIWLQTHYITYH 360		
DB	301	PREVLGTSGDYHHVDLENLAKCHEHLMQYKSKCYRFLTKGQOMIWLQTHYITYH 360		

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Db 841 SKVQPO 846

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 846 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-107-847-2
Query Match 100.0%; Score 4351; DB 3; Length 846;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFTVSCSKMSSIVDRDSSIFDGLVEEDDKDKAKRVSRNKSSEKRRDQFNVLIKELGSM 60
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